

1

SEQUENCE LISTING

<110> Meiji Seika Kaisha LTD.

<120> Triterpene hydroxylase

<130> P05160900

<150> JP 2004-049123

<151> 2004-02-25

<160> 11

<170> PatentIn version 3.1

<210> 1

<211> 32

<212> DNA

<213> Artificial

<220>

<223> primer for cDNA

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32

<210> 2

<211> 31

<212> DNA

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<220>

<223> Forward primer sequence for CYP93E1

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31

<210> 3

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31

&lt;210&gt; 8

&lt;211&gt; 1542

&lt;212&gt; DNA

&lt;213&gt; Soybean

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)..(1542)

&lt;223&gt;

&lt;400&gt; 8

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Met Leu Asp Ile Lys Gly Tyr Leu Val Leu Phe Phe Leu Trp Phe Ile	
1                      5                      10                      15	

tca acc att ctg ata cgt tcc atc ttc aag aaa cca cag cgt cta aga	96
Ser Thr Ile Leu Ile Arg Ser Ile Phe Lys Lys Pro Gln Arg Leu Arg	
20                      25                      30	

ctc cca ccg ggt cct cca att tca gta ccc ttg ctg gga cac gcg cca	144
Leu Pro Pro Gly Pro Pro Ile Ser Val Pro Leu Leu Gly His Ala Pro	
35                      40                      45	

tat ctc cgt tca ctg ctc cac caa gcc ttg tac aag cta tca ctg cgc	192
Tyr Leu Arg Ser Leu Leu His Gln Ala Leu Tyr Lys Leu Ser Leu Arg	
50                      55                      60	

tat gga ccc ttg atc cac gtc atg atc ggt tcg aag cac gtg gtg gtg	240
Tyr Gly Pro Leu Ile His Val Met Ile Gly Ser Lys His Val Val Val	
65                      70                      75                      80	

gcg tcg tcg gcg gag acg gcc aag cag atc ctc aaa acc tcg gag gag	288
Ala Ser Ser Ala Glu Thr Ala Lys Gln Ile Leu Lys Thr Ser Glu Glu	
85                      90                      95	

gca ttc tgc aac cgt ccc tta atg ata gcg agc gag agc cta acc tac	336
Ala Phe Cys Asn Arg Pro Leu Met Ile Ala Ser Glu Ser Leu Thr Tyr	
100                      105                      110	

ggc gcg gcg gac tac ttc ttc atc ccc tac ggc aca tac tgg cgg ttc	384
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Phe Ile Ala Gly Thr Asn Gly Pro Ala Ser Val Leu Glu Trp Ser Leu	
305 310 315 320	
gcg gag ctg gtg aga aac ccc cac gtt ttc aag aag gca aga gaa gag	1008
Ala Glu Leu Val Arg Asn Pro His Val Phe Lys Lys Ala Arg Glu Glu	
325 330 335	
att gag tca gtg gta ggc aaa gaa agg ctg gtc aaa gaa tca gac att	1056
Ile Glu Ser Val Val Gly Lys Glu Arg Leu Val Lys Glu Ser Asp Ile	
340 345 350	
ccc aac cta cca tac cta caa gca ttg ctg aag gaa acc cta agg ctg	1104
Pro Asn Leu Pro Tyr Leu Gln Ala Leu Leu Lys Glu Thr Leu Arg Leu	
355 360 365	
cac ccg cca acc cca ata ttc gca aga gaa gcc atg cga aca tgc cag	1152
His Pro Pro Thr Pro Ile Phe Ala Arg Glu Ala Met Arg Thr Cys Gln	
370 375 380	
gtt gaa ggc tac gac att ccg gaa aat tcc act att ttg atc agc aca	1200
Val Glu Gly Tyr Asp Ile Pro Glu Asn Ser Thr Ile Leu Ile Ser Thr	
385 390 395 400	
tgg gcc att ggt agg gat cca aat tac tgg gat gac gca ctc gag tac	1248
Trp Ala Ile Gly Arg Asp Pro Asn Tyr Trp Asp Asp Ala Leu Glu Tyr	
405 410 415	
aag ccg gag agg ttc ttg ttc tcc gac gac ccg ggc aag agc aag att	1296
Lys Pro Glu Arg Phe Leu Phe Ser Asp Asp Pro Gly Lys Ser Lys Ile	
420 425 430	
gac gtg agg ggg cag tac tat cag ctc ctg ccc ttt ggg agc ggg aga	1344
Asp Val Arg Gly Gln Tyr Tyr Gln Leu Leu Pro Phe Gly Ser Gly Arg	
435 440 445	
aga agc tgc ccc gga gcc tcg cta gcg ttg ctt gtc atg caa gca acg	1392
Arg Ser Cys Pro Gly Ala Ser Leu Ala Leu Leu Val Met Gln Ala Thr	
450 455 460	
cta gcg agt ttg atc cag tgc ttc gac tgg atc gtt aat gat ggt aaa	1440
Leu Ala Ser Leu Ile Gln Cys Phe Asp Trp Ile Val Asn Asp Gly Lys	
465 470 475 480	
aac cat cat gtt gac atg tct gag gaa ggg agg gtg act gtg ttt ttg	1488
Asn His His Val Asp Met Ser Glu Glu Gly Arg Val Thr Val Phe Leu	
485 490 495	
gcc aag cca ctc aag tgc aag cct gtt ccg cgt ttc act ccg ttc gct	1536

Ala Lys Pro Leu Lys Cys Lys Pro Val Pro Arg Phe Thr Pro Phe Ala  
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gcc tga  
 Ala

1542

<210> 9  
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 <213> Soybean

<400> 9

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Ser Thr Ile Leu Ile Arg Ser Ile Phe Lys Lys Pro Gln Arg Leu Arg  
 20 25 30

Leu Pro Pro Gly Pro Pro Ile Ser Val Pro Leu Leu Gly His Ala Pro  
 35 40 45

Tyr Leu Arg Ser Leu Leu His Gln Ala Leu Tyr Lys Leu Ser Leu Arg  
 50 55 60

Tyr Gly Pro Leu Ile His Val Met Ile Gly Ser Lys His Val Val Val  
 65 70 75 80

Ala Ser Ser Ala Glu Thr Ala Lys Gln Ile Leu Lys Thr Ser Glu Glu  
 85 90 95

Ala Phe Cys Asn Arg Pro Leu Met Ile Ala Ser Glu Ser Leu Thr Tyr  
 100 105 110

Gly Ala Ala Asp Tyr Phe Phe Ile Pro Tyr Gly Thr Tyr Trp Arg Phe  
 115 120 125

Leu Lys Lys Leu Cys Met Thr Glu Leu Leu Ser Gly Lys Thr Leu Glu

130	135	140
His Phe Val Arg Ile Arg Glu Ser Glu Val Glu Ala Phe Leu Lys Arg		
145	150	155 160
Met Met Glu Ile Ser Gly Asn Gly Asn Tyr Glu Val Val Met Arg Lys		
	165	170 175
Glu Leu Ile Thr His Thr Asn Asn Ile Ile Thr Arg Met Ile Met Gly		
	180	185 190
Lys Lys Ser Asn Ala Glu Asn Asp Glu Val Ala Arg Leu Arg Lys Val		
	195	200 205
Val Arg Glu Val Gly Glu Leu Leu Gly Ala Phe Asn Leu Gly Asp Val		
	210	215 220
Ile Gly Phe Met Arg Pro Leu Asp Leu Gln Gly Phe Gly Lys Lys Asn		
225	230	235 240
Met Glu Thr His His Lys Val Asp Ala Met Met Glu Lys Val Leu Arg		
	245	250 255
Glu His Glu Glu Ala Arg Ala Lys Glu Asp Ala Asp Ser Asp Arg Lys		
	260	265 270
Lys Asp Leu Phe Asp Ile Leu Leu Asn Leu Ile Glu Ala Asp Gly Ala		
	275	280 285
Asp Asn Lys Leu Thr Arg Glu Ser Ala Lys Ala Phe Ala Leu Asp Met		
	290	295 300
Phe Ile Ala Gly Thr Asn Gly Pro Ala Ser Val Leu Glu Trp Ser Leu		
305	310	315 320
Ala Glu Leu Val Arg Asn Pro His Val Phe Lys Lys Ala Arg Glu Glu		

325

330

335

Ile Glu Ser Val Val Gly Lys Glu Arg Leu Val Lys Glu Ser Asp Ile  
 340 345 350

Pro Asn Leu Pro Tyr Leu Gln Ala Leu Leu Lys Glu Thr Leu Arg Leu  
 355 360 365

His Pro Pro Thr Pro Ile Phe Ala Arg Glu Ala Met Arg Thr Cys Gln  
 370 375 380

Val Glu Gly Tyr Asp Ile Pro Glu Asn Ser Thr Ile Leu Ile Ser Thr  
 385 390 395 400

Trp Ala Ile Gly Arg Asp Pro Asn Tyr Trp Asp Asp Ala Leu Glu Tyr  
 405 410 415

Lys Pro Glu Arg Phe Leu Phe Ser Asp Asp Pro Gly Lys Ser Lys Ile  
 420 425 430

Asp Val Arg Gly Gln Tyr Tyr Gln Leu Leu Pro Phe Gly Ser Gly Arg  
 435 440 445

Arg Ser Cys Pro Gly Ala Ser Leu Ala Leu Leu Val Met Gln Ala Thr  
 450 455 460

Leu Ala Ser Leu Ile Gln Cys Phe Asp Trp Ile Val Asn Asp Gly Lys  
 465 470 475 480

Asn His His Val Asp Met Ser Glu Glu Gly Arg Val Thr Val Phe Leu  
 485 490 495

Ala Lys Pro Leu Lys Cys Lys Pro Val Pro Arg Phe Thr Pro Phe Ala  
 500 505 510

Ala



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 <212> DNA  
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tca acc att ctg ata cgt tcc atc ttc aag aaa cca cag cgt cta aga 96  
 Ser Thr Ile Leu Ile Arg Ser Ile Phe Lys Lys Pro Gln Arg Leu Arg  
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ctc cca ccg ggt cct cca att tca ata ccc ttg ctg gga cac gcg cca 144  
 Leu Pro Pro Gly Pro Pro Ile Ser Ile Pro Leu Leu Gly His Ala Pro  
 35 40 45

tat ctc cgt tca ctg ctc cac caa gca ttg tac aag cta tca ctg cgc 192  
 Tyr Leu Arg Ser Leu Leu His Gln Ala Leu Tyr Lys Leu Ser Leu Arg  
 50 55 60

tat gga ccc ttg atc cac gtc atg atc ggt tcg aag cac gtg gtg gtg 240  
 Tyr Gly Pro Leu Ile His Val Met Ile Gly Ser Lys His Val Val Val  
 65 70 75 80

gcg tcg tcg gcg gag acg gcc aag cag atc ctc aaa acc tcg gag gag 288  
 Ala Ser Ser Ala Glu Thr Ala Lys Gln Ile Leu Lys Thr Ser Glu Glu  
 85 90 95

gca ttc tgc aac cgt ccc tta atg ata gcg agc gag agc cta acc tac 336  
 Ala Phe Cys Asn Arg Pro Leu Met Ile Ala Ser Glu Ser Leu Thr Tyr  
 100 105 110

ggc gcg gcg gac tac ttc ttc atc ccc tac ggc aca tac tgg cgg ttc 384  
 Gly Ala Ala Asp Tyr Phe Phe Ile Pro Tyr Gly Thr Tyr Trp Arg Phe  
 115 120 125

ctg aag aag ctc tgc atg acg gag ctt ctg agc ggg aag acc ctg gag 432  
 Leu Lys Lys Leu Cys Met Thr Glu Leu Leu Ser Gly Lys Thr Leu Glu

130	135	140	
cat ttc gtg aga atc cgc gag agc gag gtg gag gcg ttc ctc aag aga			480
His Phe Val Arg Ile Arg Glu Ser Glu Val Glu Ala Phe Leu Lys Arg			
145	150	155	160
atg atg gag att tca ggc aat gga aat tac gag gtg gtg atg agg aag			528
Met Met Glu Ile Ser Gly Asn Gly Asn Tyr Glu Val Val Met Arg Lys			
165	170	175	
gag ctc ata acg cac acg aat aac atc atc acg agg atg ata atg ggg			576
Glu Leu Ile Thr His Thr Asn Asn Ile Ile Thr Arg Met Ile Met Gly			
180	185	190	
aag aag agt aat gcg gaa aac gat gag gtg gcc agg ttg agg aag gtg			624
Lys Lys Ser Asn Ala Glu Asn Asp Glu Val Ala Arg Leu Arg Lys Val			
195	200	205	
gtg agg gag gtc ggg gag ttg ctt ggg gcg ttt aac ttg ggg gat gtt			672
Val Arg Glu Val Gly Glu Leu Leu Gly Ala Phe Asn Leu Gly Asp Val			
210	215	220	
att ggg ttc atg agg cct ttg gat ctg caa ggg ttt ggg aag aag aac			720
Ile Gly Phe Met Arg Pro Leu Asp Leu Gln Gly Phe Gly Lys Lys Asn			
225	230	235	240
atg gaa act cac cac aag gtg gat gcg atg atg gag aag gtg ttg agg			768
Met Glu Thr His His Lys Val Asp Ala Met Met Glu Lys Val Leu Arg			
245	250	255	
gag cat gag gag gct agg gct aag gaa gat gct gac tct gat agg aag			816
Glu His Glu Glu Ala Arg Ala Lys Glu Asp Ala Asp Ser Asp Arg Lys			
260	265	270	
aag gat ctt ttt gat att ttg ttg aac ctc att gaa gct gat ggt gct			864
Lys Asp Leu Phe Asp Ile Leu Leu Asn Leu Ile Glu Ala Asp Gly Ala			
275	280	285	
gac aat aag ctc act aga gag agt gcc aaa gcc ttt gct ctg gac atg			912
Asp Asn Lys Leu Thr Arg Glu Ser Ala Lys Ala Phe Ala Leu Asp Met			
290	295	300	
ttc atc gcc ggc aca aac ggc ccc gca agc gtc cta gag tgg tca ctg			960
Phe Ile Ala Gly Thr Asn Gly Pro Ala Ser Val Leu Glu Trp Ser Leu			
305	310	315	320
gcg gag ctg gtg aga aac ccc cac gtt ttc aag aag gca aga gaa gag			1008
Ala Glu Leu Val Arg Asn Pro His Val Phe Lys Lys Ala Arg Glu Glu			

325	330	335	
att gag tca gtg gta ggc aaa gaa agg ctg gtc aaa gaa tca gac att Ile Glu Ser Val Val Gly Lys Glu Arg Leu Val Lys Glu Ser Asp Ile 340 345 350			1056
ccc aac cta cca tac cta caa gca gtg ctg aag gaa acc cta agg ctg Pro Asn Leu Pro Tyr Leu Gln Ala Val Leu Lys Glu Thr Leu Arg Leu 355 360 365			1104
cac ccg cca acc cca ata ttc gca aga gaa gcc atg cga aca tgc cag His Pro Pro Thr Pro Ile Phe Ala Arg Glu Ala Met Arg Thr Cys Gln 370 375 380			1152
gtt gaa ggc tac gac att ccg gaa aat tcc act att ttg atc agc aca Val Glu Gly Tyr Asp Ile Pro Glu Asn Ser Thr Ile Leu Ile Ser Thr 385 390 395 400			1200
tgg gcc att ggt agg gat cca aat tac tgg gat gac gca ctc gag tac Trp Ala Ile Gly Arg Asp Pro Asn Tyr Trp Asp Asp Ala Leu Glu Tyr 405 410 415			1248
aag ccg gag agg ttc ttg ttc tcc gac gac ccg ggc aag agc aag att Lys Pro Glu Arg Phe Leu Phe Ser Asp Asp Pro Gly Lys Ser Lys Ile 420 425 430			1296
gac gtg agg ggg cag tac tat cag ctc ctg ccc ttt ggg agc ggg aga Asp Val Arg Gly Gln Tyr Tyr Gln Leu Leu Pro Phe Gly Ser Gly Arg 435 440 445			1344
aga agc tgc ccc gga gcc tcg cta gcg ttg ctt gtc atg caa gca acg Arg Ser Cys Pro Gly Ala Ser Leu Ala Leu Leu Val Met Gln Ala Thr 450 455 460			1392
cta gcg agt ttg atc cag tgc ttc gac tgg atc gtt aat gat ggt aaa Leu Ala Ser Leu Ile Gln Cys Phe Asp Trp Ile Val Asn Asp Gly Lys 465 470 475 480			1440
aac cat cat gtt gac atg tct gag gaa ggg agg gtg act gtg ttt ttg Asn His His Val Asp Met Ser Glu Glu Gly Arg Val Thr Val Phe Leu 485 490 495			1488
gcc aag cca ctc aag tgc aag cct gtt ccg cgt ttc act ccg ttc gct Ala Lys Pro Leu Lys Cys Lys Pro Val Pro Arg Phe Thr Pro Phe Ala 500 505 510			1536
gcc tga Ala			1542

<210> 11  
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 <212> PRT  
 <213> Soybean

<400> 11

Met Leu Asp Ile Lys Gly Tyr Leu Val Leu Phe Phe Leu Trp Phe Ile  
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Ser Thr Ile Leu Ile Arg Ser Ile Phe Lys Lys Pro Gln Arg Leu Arg  
 20 25 30

Leu Pro Pro Gly Pro Pro Ile Ser Ile Pro Leu Leu Gly His Ala Pro  
 35 40 45

Tyr Leu Arg Ser Leu Leu His Gln Ala Leu Tyr Lys Leu Ser Leu Arg  
 50 55 60

Tyr Gly Pro Leu Ile His Val Met Ile Gly Ser Lys His Val Val Val  
 65 70 75 80

Ala Ser Ser Ala Glu Thr Ala Lys Gln Ile Leu Lys Thr Ser Glu Glu  
 85 90 95

Ala Phe Cys Asn Arg Pro Leu Met Ile Ala Ser Glu Ser Leu Thr Tyr  
 100 105 110

Gly Ala Ala Asp Tyr Phe Phe Ile Pro Tyr Gly Thr Tyr Trp Arg Phe  
 115 120 125

Leu Lys Lys Leu Cys Met Thr Glu Leu Leu Ser Gly Lys Thr Leu Glu  
 130 135 140

His Phe Val Arg Ile Arg Glu Ser Glu Val Glu Ala Phe Leu Lys Arg  
 145 150 155 160

Met Met Glu Ile Ser Gly Asn Gly Asn Tyr Glu Val Val Met Arg Lys  
 165 170 175

Glu Leu Ile Thr His Thr Asn Asn Ile Ile Thr Arg Met Ile Met Gly  
 180 185 190

Lys Lys Ser Asn Ala Glu Asn Asp Glu Val Ala Arg Leu Arg Lys Val  
 195 200 205

Val Arg Glu Val Gly Glu Leu Leu Gly Ala Phe Asn Leu Gly Asp Val  
 210 215 220

Ile Gly Phe Met Arg Pro Leu Asp Leu Gln Gly Phe Gly Lys Lys Asn  
 225 230 235 240

Met Glu Thr His His Lys Val Asp Ala Met Met Glu Lys Val Leu Arg  
 245 250 255

Glu His Glu Glu Ala Arg Ala Lys Glu Asp Ala Asp Ser Asp Arg Lys  
 260 265 270

Lys Asp Leu Phe Asp Ile Leu Leu Asn Leu Ile Glu Ala Asp Gly Ala  
 275 280 285

Asp Asn Lys Leu Thr Arg Glu Ser Ala Lys Ala Phe Ala Leu Asp Met  
 290 295 300

Phe Ile Ala Gly Thr Asn Gly Pro Ala Ser Val Leu Glu Trp Ser Leu  
 305 310 315 320

Ala Glu Leu Val Arg Asn Pro His Val Phe Lys Lys Ala Arg Glu Glu  
 325 330 335

Ile Glu Ser Val Val Gly Lys Glu Arg Leu Val Lys Glu Ser Asp Ile  
 340 345 350

Pro Asn Leu Pro Tyr Leu Gln Ala Val Leu Lys Glu Thr Leu Arg Leu  
 355 360 365

His Pro Pro Thr Pro Ile Phe Ala Arg Glu Ala Met Arg Thr Cys Gln  
 370 375 380

Val Glu Gly Tyr Asp Ile Pro Glu Asn Ser Thr Ile Leu Ile Ser Thr  
 385 390 395 400

Trp Ala Ile Gly Arg Asp Pro Asn Tyr Trp Asp Asp Ala Leu Glu Tyr  
 405 410 415

Lys Pro Glu Arg Phe Leu Phe Ser Asp Asp Pro Gly Lys Ser Lys Ile  
 420 425 430

Asp Val Arg Gly Gln Tyr Tyr Gln Leu Leu Pro Phe Gly Ser Gly Arg  
 435 440 445

Arg Ser Cys Pro Gly Ala Ser Leu Ala Leu Leu Val Met Gln Ala Thr  
 450 455 460

Leu Ala Ser Leu Ile Gln Cys Phe Asp Trp Ile Val Asn Asp Gly Lys  
 465 470 475 480

Asn His His Val Asp Met Ser Glu Glu Gly Arg Val Thr Val Phe Leu  
 485 490 495

Ala Lys Pro Leu Lys Cys Lys Pro Val Pro Arg Phe Thr Pro Phe Ala  
 500 505 510

Ala